RAW SEQUENCE LISTING PATENT APPLICATION US/08/663,618A

DATE: 06/16/97 TIME: 19:27:17

INPUT SET: S18386.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

1 2		SEQUENCE LISTING ENTERE
3	(1) G	eneral Information:
4 5 6	(i)	APPLICANT: Gray, Patrick W.
7 8	(ii)	TITLE OF INVENTION: Chitinase Materials and Methods
9 10	(iii)	NUMBER OF SEQUENCES: 15
11 12 13 14	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun (B) STREET: 6300 Sears Tower, 233 South Wacker Drive (C) CITY: Chicago
15 16 17 18		(D) STATE: Illinois (E) COUNTRY: United States of America (F) ZIP: 60606-6402
19 20 21 22 23 24	(V)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
25 26 27 28 29	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: (B) FILING DATE: (C) CLASSIFICATION:
30 31 32 33	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Rin-Laures, Li-Hsien (B) REGISTRATION NUMBER: 33,547 (C) REFERENCE/DOCKET NUMBER: 27866/32960
35 36 37 38 39	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 312/474-6300 (B) TELEFAX: 312/474-0448 (C) TELEX: 25-3856
40 41	(2) INFO	RMATION FOR SEQ ID NO:1:
42 43 44 45 46	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 1636 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

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47															
48	(ii) MOLI	ECULE	rype:	CDN	A								•	
49															
50	(ix) FEATURE:														
51	(A) NAME/KEY: CDS (B) LOCATION: 2 1399														
52	(B) LOCATION: 21399														
53	(iv) DDAMIDD.														
54	(ix) FEATURE:														
55	(A) NAME/KEY: mat_peptide (B) LOCATION: 651399														
56 53	(B) LUCATION: 651399														
57 58	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:														
59	·														
60	C ATG G	TG CG(ር ጥርጥ	מיים מ	ሮሮ ሞ	aa aa	ግአ ርረ	ייות יותי	ימ איז	ים מי	ויר כי	דים כי	ኮር፡ እባ	rc	46
61			g Ser												40
62	-21 -		g Ser	Val A		15 A.	La G.	Ly El	.16 M		10	eu D	eu Me		
63	21	20			•					,					
64	ATC CCA	TGG	GGC TC	г сст	GCA	AAA	CTG	GTC	TGC	TAC	TTC	ACC	AAC	TGG	94
65	Ile Pro														
66	- 5	_	•		1	•			¹ 5	•				10	
67								•							
68	GCC CAG	TAC A	AGA CA	g GGG	GAG	GCT	CGC	TTC	CTG	CCC	AAG	GAC	TTG	GAC	142
69	Ala Gln	Tyr I	Arg Gl	n Gly	Glu	Ala	Arg	Phe	Leu	Pro	Lys	Asp	Leu	Asp	
70		_	1	5				20			_		25		
71															
72	CCC AGC	CTT :	TGC AC	CAC	CTC	ATC	TAC	GCC	TTC	GCT	GGC	ATG	ACC	AAC	190
73	Pro Ser	Leu (Cys Th	r His	Leu	Ile	Tyr	Ala	Phe	Ala	Gly	Met	Thr	Asn	
74			30				35					40			
75															
76	CAC CAG														238
77	His Gln		Ser Th	r Thr	GLu		Asn	Asp	Glu	Thr		Tyr	Gln	GIu	
78		45				50					55				
79	mmc 33m		ama		N III CI	3 3 m	000	330	аша	220	3.00	ama	mm x	000	206
80 81	TTC AAT														286
82	Phe Asn	_	red ry	э гуэ	65	ASII	PIU	гуз	ьец	дуS 70	1111	теп	ьеu	мта	
83	60				0.5					70					
84	ATC GGA	ממר י	ጥርር ልል	י ייייכ	GGC	ΔርͲ	CAG	ΔAG	ጥጥር	ΔCΔ	ርልጥ	ΔТС	GΨΔ	GCC	334
85	Ile Gly														
86	75	U Ly .	TIP NO	80	-		-	_,_	85	****				90	
87															
88	ACG GCC	AAC	AAC CG	r cag	ACC	TTT	GTC	AAC	TCG	GCC	ATC	AGG	TTT	CTG	382
89	Thr Ala	Asn i	Asn Ar	g Gln	Thr	Phe	Val	Asn	Ser	Ala	Ile	Arq	Phe	Leu	
90			9	5				100				-	105		
91															
92	CGC AAA	TAC	AGC TT	r gac	GGC	CTT	GAC	CTT	GAC	TGG	GAG	TAC	CCA	GGA	430
93	Arg Lys	Tyr :	Ser Ph	e Asp	Gly	Leu	Asp	Leu	Asp	Trp	Glu	Tyr	Pro	Gly	
94	_		110	_			115		-			120		-	
95					4										
96	AGC CAG														478
97	Ser Gln	_	Ser Pr	o Ala	Val	_	Lys	Glu	Arg	Phe		Thr	Leu	Val	
98		125			*	130					135				
99															

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														. IN	<i>PUT</i>	SET: S	S18386.raw
100 101		Asp										Gln	ACC Thr				526
102 103 104	GAA	140 CGC	Сфф	ርጥጥ	ርሞር	ΔСΤ		GCG	ርምም	CCA	GCT	150 GGG	CAG	ACC	тат	GTG	574
105 106													Gln				
107 108													CTG				622
109 110 111	Asp	Ala	Gly	Tyr	Glu 175	Val	Asp	Lys	Ile	Ala 180	Gln	Asn	Leu	Asp	Phe 185	Val	
112	AAC	СТТ	ATG	GCC	TAC	GAC	TTC	САТ	GGC	тст	TGG	GAG	AAG	GTC	ACG	GGA	670
113 114 115													Lys				
116	CAT	AAC	AGC	CCC	CTC	TAC	AAG	AGG	CAA	GAA	GAG	AGT	GGT	GCA	GCA	GCC	718
117 118 119	His	Asn	Ser 205	Pro	Leu	Tyr	Lys	Arg 210	Gln	Glu	Glu	Ser	Gly 215	Ala	Ala	Ala	
120	AGC	CTC	AAC	GTG	GAT	GCT	GCT	GTG	CAA	CAG	TGG	CTG	CAG	AAG	GGG	ACC	766
121 122 123													Gln				
124	CCT	GCC	AGC	AAG	CTG	ATC	CTT	GGC	ATG	CCT	ACC	TAC	GGA	CGC	TCC	TTC	814
125	Pro	Ala	Ser	Lys	Leu	Ile	Leu	Gly	Met	Pro	Thr	Tyr	Gly	Arg	Ser	Phe	
126	235					240					245					250	
127			999	maa	ma.	ma.	a. a			ama	999	999	a a.	999		a aa	963
128 129													CCA Pro				862
130 131	****	neu ,	AIG	Der	255	Ser	vob	****	Arg	260	CIY	ALG	110	71_0	265	Cly	
132	TCT	GGC	ACT	CCA	GGC	CCC	TTC	ACC	AAG	GAA	GGA	GGG	ATG	CTG	GCC	TAC	910
133 134 135	Ser	Gly	Thr	Pro 270	Gly	Pro	Phe	Thr	Lys 275	Glu	Gly	Gly	Met	Leu 280	Ala	Tyr	
136	таπ	GAA	GTC	TGC	TCC	TGG	AAG	GGG	GCC	ACC	AAA	CAG	AGA	ATC	CAG	GAT	958
137 138													Arg 295				
139	a. a		ama	~~~	m	1 ma	mma	000	a.a		a.a	maa	GTG	999	mmm	a a m	1006
140 141													Val				1006
142	GIII	300	Val	110	- y -	116	305	7.9	пор	A.J.	01	310	V 4 1	O _T	1110	nop	
143																	
144													AAG				1054
145	_	Val	Glu	Ser	Phe	_	Thr	Lys	Val	Ser	_	Leu	Lys	Gln	Lys	_	
146	315					320					325					33♣	
147 148	CTC	aac	aaa	acc	አጥሮ	ርምሮ	TGG	GCA	ርጥር	GAC	ለ ጥጥ	СУТ	GAC	արդումո	വകവ	aac	1102
149													Asp				1102
150		1	1		335		E			340			<i>P</i>		345		
151															,		
152	TTC	TCC	TGC	AAC	CAG	GGC	CGA	TAC	CCC	CTC	ATC	CAG	ACG	CTA	CGG	CAG	1150

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153	Phe Ser Cys	s Asn Gln G	ly Arg Tyr	Pro Leu Ile	e Gln Thr Leu Arg Gln							
154		350		355	360	-						
155	a ama			ma: aaa :aa		1100						
156					CCA GAG CTT GAA GTT	1198						
157			-	_	Pro Glu Leu Glu Val							
158 159	365	•	370		375							
160	CC3 333 CC3	א ממדי מאמ מ	ממ שמש מאא	ממיד מאם מאיז	GGC CCC AGC CCT GGA	1246						
161					Gly Pro Ser Pro Gly	1240						
162	380	o Gry Grn P	385	PIO GIU MIS	390							
163	300		303		370							
164	CAA GAC ACC	3 TTC TGC C	AG GGC AAA	GCT GAT GGG	CTC TAT CCC AAT CCT	1294						
165					Leu Tyr Pro Asn Pro							
166	395	_	00	405	-							
167		_										
168	CGG GAA CGG	TCC AGC T	TC TAC AGC	TGT GCA GCG	GGG CGG CTG TTC CAG	1342						
169	Arg Glu Arc	g Ser Ser P	he Tyr Ser	Cys Ala Ala	Gly Arg Leu Phe Gln							
170		415	-	420	425							
171												
172	CAA AGC TGC	C CCG ACA G	GC CTG GTG	TTC AGC AAC	TCC TGC AAA TGC TGC	1390						
173	Gln Ser Cys	s Pro Thr G	ly Leu Val	Phe Ser Asr	n Ser Cys Lys Cys Cys							
174		430		435	440							
175	5 <u> </u>											
176			A AAGCCCCT	CC AGTCCCAGO	T TTGAGGCTGG	1439						
177	Thr Trp Asr											
178	445	5										
179			amaaamaam			- 1400						
180	GCCCAGGATC	ACTCTACAGC	CTGCCTCCT	G GGTTTTCCCT	GGGGGCCGCA ATCTGGCTC	1499						
181 182	maa aaaaamm	mamamaamam	maamma ma	a saaammama	CTCTCAGCCT TGCCTTCCT	г 1559						
183	IGCAGGCCII	ICIGIGGICI	ICCITIATC	C AGGCIIICIC	G CICICAGCCI IGCCITCCI	1 1339						
184	ጥጥጥጥርጥርርርጥ	СТССТССССТ	GCCCCTTTC	ል ሮሞሞሮሮልልልልባ	AAATCTTTGG TTTGTGCCC	1619						
185	1111010001	0100100001	000001110	A CIICCAAAA	AAATCIIIGG IIIGIGCCC	1017						
186	TCTTCCCAAA	AAAAAA				1636						
187												
188	(2) INFORMA	ATION FOR S	EQ ID NO:2	:								
189	•		_									
190	(i)	SEQUENCE C	HARACTERIS	TICS:	•							
191		(A) LENG	TH: 466 am	ino acids								
192		(B) TYPE	: amino ac	id								
193		(D) TOPO	LOGY: line	ar								
194												
195	(ii)	MOLECULE T	YPE: prote	in								
196												
197.	(XI)	SEQUENCE D	ESCRIPTION	: SEQ ID NO:	2:	•						
198	Mad 17-7 9	- Cam !!-1 :] - m *] -	al. Ph. V-4	. Ual Tau Tau Wat wi							
199	_	g Ser val A	_	GIA LUE WE	: Val Leu Leu Met Ile							
200	-21 -20		-15		-10							
20 4 5 202	Dro Tro Cl.	r Ser Ale A	la fue ten	Val Cue Tue	The Thr Ass Tes Ala							
	ETO LID GT	A вет итя W	ra nas ren	Aut che La	Phe Thr Asn Trp Ala							
203			1 .	ς	10							
203	- .5		1	5	10							
20 3 204 205	5	a Gln Glv a	_	_	10 D Lys Asp Leu Asp Pro							

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206				15					20					25		
207 208 209 210	Ser	Leu	Cys 30	Thr	His	Leu	Ile	Tyr 35	Ala	Phe	Ala	Gly	Met 40	Thr	Asn	His
211 212 213	Gln	Leu 45	Ser	Thr	Thr	Glu	Trp 50	Asn	Asp	Glu	Thr	Leu 55	Tyr	Gln	Glu	Phe
214 215 216	Asn 60	Gly	Leu	Lys	Lys	Met 65	Asn	Pro	Lys	Leu	Lys 70	Thr	Leu	Leu	Ala	Ile 75
217 218 219	Gly	Gly	Trp	Asn	Phe 80	Gly	Thr	Gln	Lys	Phe 85	Thr	Asp	Met	Val	Ala 90	Thr
220 221 222	Ala	Asn	Asn	Arg 95	Gln	Thr	Phe	Val	Asn 100	Ser	Ala	Ile	Arg	Phe 105	Leu	Arg
223 224 225	Lys	Tyr	Ser 110	Phe	Asp	Gly	Leu	Asp 115	Leu	Asp	Trp	Glu	Tyr 120	Pro	Gly	Ser
226 227 228	Gln	Gly 125	Ser	Pro	Ala	Val	Asp 130	Lys	Glu	Arg	Phe	Thr 135	Thr	Leu	Val	Gln
229 230 231	Asp 140	Leu	Ala	Asn	Ala	Phe 145	Gln	Gln	Glu	Ala	Gln 150	Thr	Ser	Gly	Lys	Glu 155
232 233 234	Arg	Leu	Leu	Leu	Ser 160	Ala	Ala	Val	Pro	Ala 165	Gly	Gln	Thr	Tyr	Val 170	Asp
235 236 237	Ala	Gly	Tyr	Glu 175	Val	Asp	Lys	Ile	Ala 180	Gln	Asn	Leu	Asp	Phe 185	Val	Asn
238 239 240	Leu	Met	Ala 190	Tyr	Asp	Phe	His	Gly 195	Ser	Trp	Glu	Lys	Val 200	Thr	Gly	His
241 242 243	Asn	Ser 205	Pro	Leu	Tyr	Lys	Arg 210	Gln	Glu	Glu	Ser	Gly 215	Ala	Ala	Ala	Ser
244 245 246	220			_		Ala 225				_	230		_	_		235
247 248 249		•	_		240	Leu	_			245	_	_			250	
250 251 252				255		-			260 •	_				265	_	Ser
253 254 255	_		270	_		Phe	4	275		_			280		_	_
256 257 258	Glu	Val 285	Cys	Ser	Trp	Lys	Gly 290	Ala	Thr	Lys	Gln	Arg 295	Ile	Gln	Asp	Gln

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